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1_	DIVLTOSPAS	LAVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	QQKPGQPPKL
51	LIYRASNLES	GIPVRFSGTG	SRTDFTLIID	PVEADDVATY	YCQQTNEDPY
-	,		SGGGSGGG		
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
			YLQLTSLTSE		
251	YWGQGTSVTV	ss (SEQID N	IO:1)		

FIG._1A

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGGCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	${\tt ATGTCCTGCA}$	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	${\tt GTGCTTCTAA}$	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTCGTACTG	$\mathtt{ATTTTACC}\mathbf{CT}$	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGCGGCG	$\tt GTGGTAGCGG$	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	$\mathtt{TCTGAAGT}$ \mathtt{GC}	AGCTGCAGCA	GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGA.AA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCAC TG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	$\mathtt{TGACTTCC}\mathtt{CT}$	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	$\tt GGCTACTA_TG$	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGC (SEC) ID NO:3)

FIG._1B

TPVSEKQL AEVVANTITP LMKAQSVPGM AVAVIYQGKP

301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA

351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW

401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW

451 INVPKAEEAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM

501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF

551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGSYVAF IPEKQIGIVM

602 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:11)

FIG._1C

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1	ACACCGGTGT	CAGAAAAACA	GCTGGCGGAG	GTGGTCGCGA	ATACGATTAC
51	CCCGCTGATG	AAAGCCCAGT	CTGTTCCAGG	CATGGCGGTG	GCCGTTATTT
101	ATCAGGGAAA	ACCGCACTAT	TACACATTTG	GCAAGGCCGA	TATCGCGGCG
151	AATAAACCCG	TTACGCCTCA	GACCCTGTTC	GAGCTGGGTT	CTATAAGTAA
201	AACCTTCACC	GGCGTTTTAG	GTGGGGATGC	CATTGCTCGC	GGTGAAATTT
251	CGCTGGACGA	TGCGGTGACC	AGATACTGGC	CACAGCTGAC	GGCAAGCAG
301	TGGCAGGGTA	TTCGTATGCT	GGATCTCGCC	ACCTACACCG	CTGGCGGCCT
351	GCCGCTACAG	GTACCGGATG	AGGTCACGGA	TAACGCCTCC	CTGCTGCGCT
401	TTTATCAAAA	CTGGCAGCCG	CAGTGGAAGC	CTGGCACAAC	
451	GCCAACGCCA	${\tt GCATCGGTCT}$	TTTTGGTGCG	CTGGCGGTCA	AACCTTCTGG
501	CATGCCCTAT	GAGCAGGCCA	TGACGACGCG	GGTCCTTAAG	CCGCTCAAGC
551	TGGACCATAC	CTGGATTAAC	GTGCCGAAAG	CGGAAGAGGC	GCATTACGCC
601	TGGGGCTATC	${\tt GTGACGGTAA}$	AGCGGTGCGC	GTTTCGCCGG	GTATGCTGGA
651	TGCACAAGCC	${\tt TATGGCGTGA}$	AAACCAACGT	GCAGGATATG	GCGAACTGGG
701	TCATGGCAAA	CATGGCGCCG	GAGAACGTTG	CTGATGCCTC	ACTTAAGCAG
751	GGCATCGCGC	TGGCGCAGTC	GCGCTACTGG	CGTATCGGGT	CAATGTATCA
801	GGGTCTGGGC	TGGGAGATGC	TCAACTGGCC	CGTGGAGGCC	AACACGGTGG
851	TCGAGACGAG	TTTTGGTAAT	GTAGCACTGG	CGCCGTTGCC	CGTGGCAGAA
901	GTGAATCCAC	CGGCTCCCCC			ATAAAACGGG
951	CTCTACTGGC	GGGTTTGGCA	GCTACGTGGC	CTTTATTCCT	GAAAAGCAGA
1001					GGCACGCGTT
1051	GAGGCGGCAT	ACCATATCCT	CGAGGCGCTA	CAG (SEQ ID	NIO:12)

FIG._1D

1	DIVLTQSPAS	LAVSLGORAT	MSCRAGESVD	IFGVGFLHWY	OOKPGOPPKL
51	LIYRASNLES	GIPVRFSGTG	SRTDFTLIID	PVEADDVATY	YCOOTNEDPY
101	TFGGGTKLEI	K <i>GGGGSGGG</i>	SGGGSGGGG	SGGGGSGGGG	<i>S</i> EVOLOOSGA
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
201	YVPKFQGKAT	ITADTSSNTA	YLQLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251	YWGQGTSVTV	SSTPVSEKQL	AEVVANTITP	LMKAQSVPGM	A VAVIYQGKP
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	OPOWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	MIAMVWIAMC
501	APENVADASL	KOGIALAOSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFG S YVAF	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALO (SEQID	NO:2)	

FIG._1E

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1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGGCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTCGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGCGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	${\tt TGGCGGTGGC}$	TCTGAAGTGC		GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA		CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGAAAG
851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG	TTATTTATCA	GGGAAAACCG
901	CACTATTACA	CATTTGGCAA	GGCCGATATC	GCGGCGAATA	AACCCGTTAC
951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG	CTACAGGTAC
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	TCAAAACTGG
1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	ACGCCAGCAT
1251	CGGTCTTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG	CCCTATGAGC
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	CCATACCTGG
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG	GCTATCGTGA
1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	CAAGCCTATG
1451	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT	GGCAAACATG
1501	GCGCCGGAGA	ACGTTGCTGA	TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1551	GCAGTCGCGC	TACTGGCGTA	. TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1601	AGATGCTCAA	CTGGCCCGTG	GAGGCCAACA	CGGTGGTCGA	
1651	GGTAATGTAG	CACTGGCGCC			
1701	TCCCCCGGTC	AAAGCGTCCT		AACGGGCTCT	
1751	TTGGCAGCTA	CGTGGCCTTT		AGCAGATCGG	
1801	CTCGCGAATA	CAAGCTATCC		CGCGTTGAGG	CGGCATACCA
1851	TATCCTCGAG	GCGCTACAG	(SEQ ID NO:4))	

FIG._1F

1	DIVLTOSPAS	LSVSLGORAT	MSCRAGESVD	IFGVGFLHWY	QOKPGOPPKI
51	LIYRASNLES	GIPVRFSGTG	SGTDFTLIID	PVEADDVATY	YCQQTNEDPY
	TFGGGTKLEI				
	ELVEPGASVK				
	YVPKFQGKAT				
	IVIII QUILI				

251 YWGQGTSVTV SS (SEQ ID NO:5) FIG._2A

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1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	${\tt CTGTCTGTTT}$	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGC (SEC	Q ID NO:6)

FIG._2B

262	TPVSEKQL A	EVVANTITP LI	MAAQSVPGM AT	/AVIYQGKP	
301	HYYTFGKADI	${\tt AANKPVTPQT}$	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551				$\mathtt{TGGFG}\mathbf{A}\mathtt{YVAF}$	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALQ (SEQ ID	NO:13)	

FIG._3

1	DIVLTOSPAS	LSVSLGQRAT	MSCRAGESVD	IFGVGFLHWY	OOKPGOPPKL
51	LIYRASNLES	GIPVRFSGTG	SGTDFTLIID	PVEADDVATY	YCOOTNEDPY
101	TFGGGTKLEI	KGGGGSGGG	SGGGGSGGG	SGGGGSGGG	SEVQLQQSGA
151	ELVEPGASVK	LSCTASGFNI	KDTYMHWVKQ	RPEQGLEWIG	RIDPANGNSK
201	YVPKFQGKAT	ITADTSSNTA	YLOLTSLTSE	DTAVYYCAPF	GYYVSDYAMA
251	YWGQGTSVTV	SSTPVSEKQL	AEVVANTITP	LMKAQSVPGM	AVAVIYQGKP
301	HYYTFGKADI	AANKPVTPQT	LFELGSISKT	FTGVLGGDAI	ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD	LATYTAGGLP	LQVPDEVTDN	ASLLRFYQNW
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451	INVPKAEEAH	YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501	APENVADASL	KQGIALAQSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGSYVAF	IPEKQIGIVM
601	LANTSYPNPA	RVEAAYHILE	ALO (SEQID	NO:7)	

FIG._4A

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101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAACTG 151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC 151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC 151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGATCCCGG TACGTTTCTC 152 CAGACGATGT TGCCACCTAC TATTGCCAG AGACCAACGA GGATCCGTAC 153 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC 154 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC 155 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC 156 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCTAGC 157 CAGACGATGT AGCGGTGGCG GTGGTACCGA TGCGGTGGTGC AGCGTGGTGC AGCGTGGTGC AGCGTGGTGC TGCGGTGCG AGCGTGGTGC AGCGTGCTGC TGCGGTGCC TCTCAAGTGC AGCTCCAGCA GTCCGGTGCC 156 CAGACCACTA AACACCCT ACATGCACTA GGTGAAACAA CGCCCCGGAAC 157 CACACCTACAACACCA AACACCACACAACACAAAA CTGCCTCTCCGCACACGA ACACCCACACACACAACACA	1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC 201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG 251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC 301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG 351 TGGTGGTGGT AGCGGTGGC GTGGTAGCGG TGGCGGTGCC AGCGGTGGTG 401 GTGGCTCTGG AACCGGGCGC TCTGAAGTGC ACTGCTGCC AGCCGTGCG 451 GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGGCGACA GTCCGGTGCG 451 GAGCTCTGTA AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CGCCCGGAAC 551 AGGGTCTGGA GTGGATCGGT CGCATCGGT GGTGAACCAA CGCCCGGAAC 651 TACACACTA AAGGACACCT ACATGCACTG GGTGAACCAA CGCCCGGAAC 651 TACGTGCCAA AATTCCAGGG TAAACCAACC ATCACTGCTG AAACCACCAC 651 TACACACTGC TACCTGCAGC TGACTTCCT GACTAGCGAA GACACCCCGC 701 TTTATTACTG CGCTCCTGTTC GGCTACTAGT TCAGCGGAAC GACACCGCGC 701 TACTGGGGT AGGGCACCTC TGTTACCTTT TCTAGCACAC CGCTGTCAGA 801 AAAACAGCTG GCGGAGGTG TCGCGAATAC GATTACCCCG CTGATGAAA 801 CACTATTACA CATTTGGCAA GCCCGATATC GCGGCGAATA AACCCGGTGC 901 CACTATTACA CATTTGGCAA GCCCGATATC GCGCGGAATA AACCCGTTAC 901 CACTATTACA CATTTGGCAA GCCCGATATC GCGCGGAATA AACCCGTTAC 901 GCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCCCT GGGACGATAC 1101 TATGCTGGAT CTCGCCACAT ACACCGCTG CGCCTGCCC CTACAGGGTA 1101 TATGCTGGAT CCCGCCACA ACCCCCTGC TGCGCTTTAT TACAGCGGC 1101 CAGCCGCAGT GCGAGACAC TCCGCCCG CTACAGGGTA 1251 CGGTCTTTTT GGTCGCCTG CGCTCACCT TCGGCCTTTA TCACACGGCT 1301 AGGCCATGA CACCGGGTC CTTAAGCCGC CTACAGGTAC 1301 AGGCCATGA CACCGGGTA CCCGCTGC CCCATACCGGTG 1301 AGGCCATGA CACCGGGTA CCCGCTGC CCCATACCGGTG 1301 AGGCCATGA CACCGGGTA CCCGCTGC CCCATACCGGGT 1301 AGGCCATGA CACCGGGTA CACCGCTGC CCCATACAGGTA 1551 GGGTAAAAC CACGGGTA CCCGCTGC CTTACGGCTA CCCATACCTGG 1551 GGGTAAACC CACGGGTA CCCGCTGA CCCGCGTAACC CCCATACCTGG 1551 GGGCCGGA ACGTTGCTG GAGGCCAACA CCGGGTACA CCCATACCTGG 1551 GCGCCGGAAAC CACGGGGT TCGCGCTTT ATCGCCGGC GCCGCTTTACGGCGC 1551 GCAGTCCGC TAC	51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG 251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC 301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG 351 TGGTGGTGGT AGCGGTGGC GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG 401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG 451 GAGCTCGTTG AACCGGGCGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG 451 GAGCTCGTTG AACCGGGCGC TCTGTAAA CGTGCTTTGCA CTGCATCTGG 501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC 551 AACACTGCA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACAGCAAA 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACAGCAACA 601 TACAGTGCAA AATTCCAGGG TGAACTCATTGCT AACAGCAACA 701 TTTATTACTG GCCTCCGTTC GGCTACTGT TCAACGGCAAC 801 AAAACAGCTG GCGAGGTGG TCGCAATAC GATTACCCGC TGAATACGCAAC 801 AAAACAGCTG GCGAGGTGG TCGCAATAC GATTACCCGC CTGATGAGG 801 AAAACAGCTG GCGAGGTGG TCGCGAATAC GATTACCCGC CTGATGAAG 801 CACTATTACA CATTTGGCAA GGCGTAGCC TTATTTATCA GGGAAAACCC 901 CACTATTACA CATTTGGCAA GGCGTAGCCG TTAATTTATCA GGGAAAACCC 901 CACTATTACA CATTTGGCAA GGCGTAGCCG TTAATTTATCA GGGAAAACCC 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCCCT TCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATAC 1101 TATGCTGGAT ACTGGCCACA GCTGACGGC AAGCAGTGCC GTACAGGTACC 1101 TATGCTGGAT CTCGCCACCT ACACCGCTG CAACACTTCCGCGCG 1101 TATGCTGGAT CTCGCCACCT ACACCGCTG CAACACTGCC CTACAGGTAC 1251 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTA TCAAAACCTG 1251 CGGATGAGG CACGCGGTC CTTAACCCGC TGCGCTTTAC TCAAGCAGAC 1251 CGGATGAGC CACGGGTC CTTAACCCGC TCCCTGCG CTACAGGTAC 1251 CGGTCTTTTT GGTGCCTGC CGGTCAAACC TTCGCGGCG 1351 ATTAACGTGC CAAAGCCGGT CTTAACCCGC TCCATGCG CCTATCCTGG 1451 CGGTTAAAGC GACGCGGTC CTTAACCCGC TCCAGCTGC CCTATCCGGC 1551 GCGCCGGAAA CCTTGCCGGTA GCTGGCCTTTACGCCA ACGCCTATCCTGG 1551 GCGCCGGAAA CCTTGCCGGTC CTTAACGCGC TCAACCTGG CCAAACCTGC 1551 GCGCCGGAAAC CAACGCGTT CCGCGGTAT GCCGCAACATC 1551 GCGCCGGAAAC CAACGCGTT CCGCGGTAT GCCGCTACAC CGGTGGCCAACATC 1551 GCGCCGGAAAC CAACGCGCT TCACGCGGTAT TCGCCCGGC TCACAGGGTTT 1551 GCGCCGGAAAC CAACGCGCT TCACGCGCT TCGGGCTAACC TCGGGCTAACC TCGGGCTAACC TTGGCGGTAACC TTGGCG	101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC 301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG 351 TGGTGGTGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGCC AGCGGTGGCG 401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA CTCCCGGTGCG 451 GAACTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTGTGCACCA CTGCATCTGG 501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA 601 TACGTGCCAA AATTCCAGGG TAAACCAACC ATCACTGCTG ATACCTCCTC 651 TAACACTGCT TACCTGCAGC TGAATTCCCT GACTAACGG TAACACGCCGG 701 TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGAAT CGCACCCGCGG 701 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCGAA CGCACCGCGG 801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAA 851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGCAAAACA 851 CCCAGTCTGT TCCAGGCATG GCGGTTGCCG TTATTTATCA GGGAAAACC 901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGT AAATTTCCCT GGACGATTAC 1051 GTGACCAGAT ACTGGCCACT ACACCCGTGG CGGCCTACCAGAC TCCACTACCTGC 1051 GTGACCAGAT ACTGGCCACA GCTGACGGC AAACTTCCCT GGACGATCCC 1101 TATGGTGGAT CTCGCCACCT ACACCCCTGC CTGCCTTCCT GCACCATTCC 1101 TATGCTGGAT CTCGCCACCT ACACCCCTGC CTGCCTTCCTTA TAAAACCTTCC 1201 CAGCCGCAGT GAAAGCCTGG CACACCCCTGC CTCCTCTCT TAAAACCTGC 1301 AGGCCATGAC GAAAGCCTGG CACACCCTGC TCCGCTTCC CTCCTTTA TAAAACCTGG 1301 AGGCCATGAC GAAAGCCTGG CACACCCTGC TCCGCTTCC CTCAAAACCTGG 1301 AGGCCATGAC GAAAGCCTGG CACAACCGCTT TCTAGGCCA ACGCCACATACCTGG 1301 AGGCCATGAC CACGGTTAC GCCCCCTGC TCCACTTA CACGCCTGG CTAAAACCTGG 1301 AGGCCATGAC CACGGTTAC CCCCCTGC TCCACTTA CACGCCTGG CTAAAACCTGG 1301 AGGCCATGAC CACGGTTCCCTTC TCTAGACCTGG CCTATCCTGG 1301 AGGCCATGAC CACGGCTA TCCGCCTGC TCCACTTA ACCCCTGG CTAAAACCTGG 1301 AGGCCATGAC CACACCTGGCC TCTAAACCTGG CCTATCCTTTA 1451 GCGCGGAAACCC TCCCCTCC CCGCCTACAAC CCTATCCTGG 1351 ATTAACGTGC CACACCTGCTG CACACCCTGC TCCACTTA AACCAGGGCA TCCCCTGC 1551 GCGCCGGAAACCC CACACCCTGC CACACCCTGGCC CTTACAGGTA ACCCCGCTA GCCCTATACCACGC TCCCCTCT GCGCCTATACCACGC TCCCCTCTC GCGCTAA	151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG 351 TGGTGGTGGT AGCGGTGGC GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG 401 GTGGCTCTGG TGGCGGTGGC TCTGAAAGTGC AGCTGCAGCA GTCCGGTGCG 451 GAGCTCGTTG AACCGGGCGC TTCTGTAAAA CTGTCTTGCA GTCCAGTACG 501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC GGTGAACAGA CTACACGCACA 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC 651 TAACACTGCT TACCTGCACC TGACTTCCCT GACTAGCGAA GCACACGCGG 701 TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATA CGCAATGGCC 751 TACTGGGGTC AGGGCACCT TGTTACCGTT TCTGAGCACA CGGTGTCAGA 801 AAAACAGCTG GCGGAGGTG TCGCGATAC GACTAGCCC CTGATGACAC CGGTGTCAGA 851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTACC 901 CACTATTACA CATTTGGCAA GGCCGATAAC GATTACCCC CTGATGAAAC 951 GCCTCAGAC CTGTTCGAC TGGCTATATT CACGGGATA AACCCGTTAC 951 GCCTCAGAC CTGTTCGAC TGGCGATAAC GACTAACC TCACGGCGC 1001 TTTTAGGTGG GAATGCCATT GCTCGCGGTG AAATTTCCC GGCGAATAC 101 TATGCTGGAT CTCGCCACCT ACACCGCTG CGGCGTGCC GTACAGGTCC 1051 GTGACCAGAT ACTGGCCACA GCTGACGGC AAGCAGTGCC GACCGATCC 1051 GTGACCAGAT ACTGGCCACA GCTGACGGC CTACAGGTAC 1101 TATGCTGGAT CTCGCCACCT ACACCGCTG CGGCCTGCC GTACAGGTAC 1201 CAGCCGCAGT GAAGCCTTG CCCCCTCC TCGCTTTAT AAACTCCT GGACGATCC 1201 CAGCCGCAGT GGAAGCCTG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTTTTTT GGTGCGCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGCTTTTT GGTGCGCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCATAAC GCCTCCTGC TGCTTTTAT CCCAGGCC 1301 AGGCCATGAC GAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCAAAAC CAACGGGT CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCAAAAC CAACGGGT CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGCCGGAAAC CAACGGGT CTTAAGCCG TCCATAGAGC 1301 AGGCCATGAA CATGCGCT CACAACGCGT TACAGCTGG CCTATAGAGC 1301 AGGCCAGGA ACGTGCGA AGAGCCAAC CACAGCGT TCAAGCTGG 1301 AGGCCAGGA ACGTGCG TCTAAACCTGG CACAACAGC CTAACAGGGT CTTACGCCA ACGCCAGCAT 1451 GCGCCGGAAAC CAACGGGCA AGAGCCAAC CACAGCGT TCAAGCTGG CTAACACGGT 151 ATTAACGTG CAAACGGGA AGAGCCAAC CAGGCCAACA CACGCGGC TACCGGGC TACCGGGC TACCGGGC TACCGGGC TACCGGGC TACCGGGC TACCGGGC TACCGGGC TACCGGGG	201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGCC AGCGGTGGTG A01 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG A51 GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG 501 TTTCAACATT AAGGACCACT ACATGCAGTC GGTGAAACAA CGCCCGGAAC 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA 601 TACGTGCCAA AATTCCAGGG TAAAGCAACA ATCACTGCTG ATACCTCCTC 651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG 701 TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATTA CGCAATGGCC 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA 801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAG 851 CCCAGTCTGT TCCAGGCATG CGGGTGCCG TTATTTATCA 901 CACTATTACA CATTTGGCAA GGCCGATTAC GCGGCAATAC GATTACCCG CTGATGAAG 901 CACTATTACA CATTTGGCAA GGCGGTGCCG TTATTTATCA GGGAAAACCG 901 CACTATTACA CATTTGGCAA GGCGGTGCCG TTATTTATCA GGGAAAACCG 901 CACTATTACA CATTTGGCAA GCCGGTGCCG TTATTTATCA GGGAAAACCG 901 CACTATTACA CATTTGGCAA GCCGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCAT GCTCGCGGTG AAATTTCGCT GGACGATTCC 951 GCGCCAGAT ACTGGCCACA GCTGCGGGT AAATTTCGCT GGACGATTCC 1051 GTGACCAGAT ACTGGCCACA GCTGCCGGT CAAGCATGCC CTACAGGTAC 1051 CGGATGAGGT CACGGATAAC GCCTCCTGC TGCGCTTTTA TCAAAACTGC 1051 CGGATGAGGT CACGGATAAC GCCTCCTGC TGCGCTTTTA TCAAAACTGC 1101 CAGCCGCAGT GCAGGATAAC GCCTCCTGC TGCGCTTTTA TCAAAACTGC 1201 CAGCCGCAGT GCAGAAGCCTG CACAACCGCT TTCTGGCATC CCCTATGAGC 1201 CAGCCGCAGT GGAAGCCTGG CGGCTCCTGC TCCGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GCAGAAGCCAC TTCTGGCATT TCAAAACTGG 1201 CAGCCGCAGT GCGCGTTT CGCCCACT TACGCGCT CCCTATCAGCC 1301 AGGCCATGAC GACGCGGA CACACCGCT TTCTGGCATC CCCTATCTGG 1401 CGGTAAAACC GACGCGAA AAGAGCCCAA ACGCCAACGCT 1501 GCGCCGAGAA ACGTGCGA TCGCGGTTT CGCCGGTTT AAGCCTGC CTAACCTGG 1501 GCGCCGAGA ACGTGCCG TTCAGGGGATAAC CAAGCCTATG 1501 GCGCCGAGA ACGTGCGA TCGGGCTAT GCCGGTTTT AAGCAGGA ACGGCAACAC CGGTGTCAA ACCGCGCA TCGGGCCTTTAACCTGG GCAAACACAC CGGGTCAACAC CGGGTCAACACAC CGGGTCAACACAC CGGGTCAACACAC CGGGTCAACACAC CGGGTCAACACAC CGGGTCAACACAC CGGGTCCAACACAC CGGGCTACCACACACACACACACACACACACACACACACA	251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG 451 GAGCTCGTTG AACCGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG 501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC 651 TAACACTGCT TACCTGCAGG TGACTTCCCT GACTAGCGA ATCACTGCTGA 701 TTTATTACTG CGCTCCGTTC GGCTACTGT TCAGCGATTA CGCAATGGCC 751 TACCTGCGGC AGGGCACCTC TGTTACCGTT TCAGCGATTA CGCAATGGCC 751 TACACACTGC TCGGGGGAGCTG TCGCGAATAC GATTACCCCC CTGATTGAAA 801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCC CTGATGAAAG 851 CCCAGTCTGT TCCAGGCATG GCGGGATATA GGCAAAACCG 901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGATTAT GGGGCGAATA AACCCGTTAC 1001 TATGCTGGAT ACTGGCCACA GCTGACGGG AAAATTTCGCT GGACGATGCG 1001 TATGCTGGAT CTCGCCACCT ACACCGCTG CGGCCTGCCG CTACAGGTAC 1101 CAGCCGCAGT GCGGAAGCC CTGCCGCG CTACAGGTAC 1201 CAGCCGCAGT GCAGAACCCTG CGGCCTGCCG CTACAGGTAC 1201 CAGCCGCAGT GGAAGCCTGG CACAACCGCT TCTTCAGCCA ACGCCAGCAT 1251 CGGATCAGAC GACGGGATAC GCCTCCTGC TGCGCTTTTA TCAAAACCTGG 1201 CAGCCGCAGT GAAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGATCAGAC GACGCGGTC CTTAAGCCGC TCACAGGTAC 1351 ATTAACGTGC CACAAAGCCGA TACCCGGC TCACAGCTAC 1451 GCGCTGAAAAC CACCGCTTT CGCCCTTC TGCGCTTTTA TCAAAACCTGG 1351 ATTAACGTGC CGAAAGCCGA AGAGCCCAT TACGCCGG GCTATCCTTGG 1451 GCGCGGAAA ACGTTGCTGA ACGCGCAT TACGCCTGG GCTATCCTTGG 1551 GCGCCGGAA ACGTTGCTGA TCGCGCCAT TACGCCGA CAAGCCTAGC 1551 GCGCCGGAA ACGTTGCTGA TCGCGCCAT TACGCCGC TCGGGCTTTCAGCCA ACGCCTTGGA 1551 GCGCCGGAAA ACGTTGCTGA TCGCGCCAT TACGCCGC TCGGGCTTGCA 1551 GCGCCGCGC TACTGGCGCA TCGGGCCAT TACGCCGC TCGGCTTGCA 1551 GCGCCGCGC TACTGGCGCA TCGGGCCAT TACGCCGC TCGGCCTTGCATCATCATCATCATCATCATCATCATCATCATCATCATC	301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
451 GAGCTCGTTG AACCGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG 501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC 651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG 701 TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATA CGCAATGGCC 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA 801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG 851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG 901 CACTATTACA CATTTGGCAA GGCCGATATC GCGCGAATA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGTG AAATTTCGCT GGACGATCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGTG AAATTTCGCT GGACGATCG 1051 GTGACCAGAT ACTGGCCACA GCTGACGGC CACACAGTGC CGGCTTTTC 1101 TATGCTGGAT CTCGCCACCT ACACCGCTGC CGGCCTGCCG CTACAGGTAC 1201 CAGCCGCAGT GACACCCTC CACACCGCTG CGGCCTTTAC 1201 CAGCCGCAGT GACACCCTC CACACCCTC CTCCCTGC CTACAGGTAC 1301 AGGCCATGAC GACACGCGT CTTAACCCAC ACGCCAGCAT 1251 CGGTTTTTT GGTCGCGTG CACAACCGCTT CTCTGGCAC CTTACACGCTA 1301 AGGCCATGAC GACACGCGT CTTAACCCAC TCCAGCATG 1301 AGGCCATGAC CACACGCGTC CTTAACCCAC TCCAGCATG 1401 CGGTAAAACC GACGCGGTC CTTAACCCAC TCCAGCTATG 1401 CGGTAAAACC GACGCGGTC CTTAACCCAC TCCAGCTATG 1451 GCGCCGGAA ACGTTGCTGA ACGCCAACC TCCAGCTATG 1451 GCGCCGGAA ACGTTGCTGA TCCCCACAC TCCAGCTATG 1451 GCGTGAAAAC CAACGTGA AGGGCGCAT TACGCCTGGG GCTATCCTGG 1501 GCGCCGGAA ACGTTGCTGA TCCCCCTGC TCAAGCTGA CCCTATCGTGA 1401 CGGTAAAACC GACCGTGCA TCCCCTGC TACAGCTGC 1501 GCGCCGGAA ACGTTGCTGA TCCGCGCTAT TACGCCAACAC CTGGGCTCATGACC 1501 GCGCCGGAA ACGTTGCTGA TCCGCGCTATGAGC 1501 GCGCCGGAA ACGTTGCTGA TCCGCGCTATGAGC 1501 GCGCCGGAAACC TTCTGGCGTA TCCGCGTGA ACCATACCTGG 1501 GCGCCGGAA ACGTTGCTGA TCCGCGCTGAACC TTCGGGCTAT TACGCCAACA CGGGGTAT TCCGCGTGA ACCATACCTGG 1501 GCGCCGGAA ACGTTGCTGA TCCGCGCTGAACAC CGGTGGTCAACA ACCAGCTTATACACCTGG 1501 GCGCCGGAA ACGTGCCCTG GAGCCACA CGGTGGTCAACA ACCAGCTTTACACCGC 1501 TTCGCCCGGTC AAAGCGTAA AACCCGGCTAACAC TTCGGCGGGT TCCCCGTG GAGCACA CGGTGGTCAACA	351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC 651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG 701 TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATTA CGCAATGGCC 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA 801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG 851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG 901 CACTATTACA CATTTGGCAA GGCCGATTAT GCGGGAATAA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATGCC 1051 GTGACCAGAT ACTGGCCACA GCTGACGGC AAGCAGTGGC CAGCAGTACC 1151 CGGATGAGGT CACCGCACA GCTGACGGC AAGCAGTGC CAGCAGTACC 1251 CGGATGAGGT CACCGCACA GCTGACCGGC TGCCGCG CTACAGGTAC 1251 CGGATGAGGT CACCGGATAAC GCTCCCTGC CGCCTGCCG CTACAGACTGC 1301 AGGCCATGA CGCGCATAC CCTCCCTGC CTACAGACTGC 1301 AGGCCATGAC GAAGCCTGG CACAACGCGT TTTACCGCCA ACGCCAGTA 1251 CGGTCTTTTT GGTGGCGTG CACAACCGCT TTCTGGCCAT ACCCCTGCA ACGCCAGTA 1251 CGGTCTTTTT GGTGGCGTG CACAACCGCT TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGT CTTAAGCCGC TCAAGCTGA 1401 CGGTAAAGCG GACGCGGTC CTTAAGCCGC TCAAGCTGGA CCCTATGAGC 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGAA TCCCCTTGG 1551 GCGCGGAGA ACCTTGCTGA TGCCTCACTT AAGCAGGGA CCATACCTTG 1451 GCGCGAAAC CAACCTGCA GACGCCATT TCCGCCTGGC TCAAGCTATG 1551 GCAGTCCACA CTGGCCCTT TCCGCCTATGAGC CGGTCAACC TTCTGGCAG ACCACACACACACACACACACACACACACACACA	401	GTGGCTCTGG	${\tt TGGCGGTGGC}$	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC 651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG 701 TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATTA CGCAATGGCC 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACACC CGGTGTCAGA 801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG 851 CCCAGTCTGT TCCAGGCATG GCGGTGCCGA TCAGTCACA CGGTGTCAGA 901 CACTATTACA CATTTGGCAA GGCCGATATC GCGCGAATA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGTCTAT AAGTAAAACC TTCACCGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGT AAATTTCGCT GGACGATGCG 1051 GTGACCAGAT ACTGGCCACA GCTGACGGC CGGCCTGCC CTACAGGTAC 1101 TATGCTGGAT CTCGCCACCT ACACCGCTG CGGCCTTTAT ACGCAGTAC 1251 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTAT ACGCAGCAT 1251 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTAT ACGCAGCAT 1251 CGGTCTTTTT GGTGCGCGCG CACAACCGCT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGCGGC CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAACCTGG 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGA CCCTATGAGC 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGG GCTATCGTGA 1401 CGGTAAAACC GCCGCGGTT CCGCGGTTAT GCCCAACCTG 1551 GCGTGAAAAC CAACGTGCA GATATGGCGA ACGCGGGTCAT GCCCATACCTGG 1551 GCGTGAAAAC CAACGTGCA GATATGGCGA ACGCGGGTCAT GCCCATACCTGG 1551 GCAGTCCACA CACGTGCA GATATGGCGA ACGCGGCAT TCCGCCTGGC 1551 GCAGTCCACA CCGCGGTAT GCCAGACCAT TCGCCTAGC 1551 GCAGTCCACA CCGCGGTAT GCCAAACCATG 1551 GCAGTCCACA CCGCGGTAT TCGGCTCACT AAGCCAGGCA TCGCGCTGGC 1551 GCAGTCCACA CCGGTGCAACC CGGTGCCA TCGCGCTGGC 1551 GCAGTCCACA CCGGTCAAC CGGTGCAACCATG 1551 GCAGTCCACA CCGGGTCA TCGGGTCAACCATG 1551 GCAGTCCACA CCGGGTCA TCGCGCTGGC 1551 GCAGTCCACA CCGGGTCAAC CGGTGGCAACACATG 1551 GCAGTCCACA CGGGCCAACA CGGGTCAACACATG 1551 GCAGTCCACA CGGGCCAACA CGGGTCAACACATG 1551 GCAGTCCACA CAGGGCCAACA CGGGGTCAACACATG 1551 GCAGTCCACA CAGGCCAACA CGGGTCAACACATG 1551 GCAGTCCACA CAGGGCCAACA CGGGTCAACACACGGCAACACACACGGCAACACACACACGGCAACACACACACACACACACACACACACACACACACACAC	451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
601TACGTGCCAAAATTCCAGGGTAAAGCAACCATCACTGCTGATACCTCCTC651TAACACTGCTTACCTGCAGCTGACTTCCCTGACTAGCGAAGACACCGCGG701TTTATTACTGCGCTCCGTTCGGCTACTATGTCAGCGATTACGCAATGGCC751TACTGGGGTCAGGGCACCTCTGTTACCGTTTCTAGCACACCGGTGTCAGA801AAAACAGCTGGCGGAGGTGGTCGCGAATACGATTACCCCGCTGATGAAAG851CCCAGTCTGTTCCAGGCATGGCCGGTGGCCGTTATTTATCAGGGAAAAACCG951GCCTCAGACCCATTTGGCAAGGCGGATATCGCGGCGAATAAACCCGTTAC951GCCTCAGACCCTGTTCGAGGTGGGTCTATAAAGTAAAACCTTCACCGGCG1001TTTTAGGTGGGGATGCCATTGCTCGCGGTGAAATTTCGCTGGACGATGCG1051GTGACCAGATACTGGCCACCTACACCGCTGGCGGCCTGCCGCTACAGGTAC1101TATGCTGGATCTCGCCACCTACACCGCTGGCGGCCTGCCGCTACAGGTAC1201CAGCCGCAGTGGAAGCCTGGCGCTCCCTGCTCTTACGCCAACGCCAGCAT1251CGGTCTTTTTGGTGCGCTGGCCTAAACCTGGCCTATCCTGGCCTATCCTGG1301AGGCCATGACGACGCGGGTCCTTAAGCCGCTCAAGCTGGACCATACCTGG1351ATTAACGTGCGGACGCGGTTCGCGGGTATGCTGGATCCACAAGCCTATG1451GCGTGAAAACGTGCGCTTCGCGGGGTATGCTGGGTCACAAACATG1551GCGCTGAAACTGGCTGGAACTGGGCTAACTGGGTCAAACTGGGTCGACTGGCTGGG1551GCAGTCCAACTGGC	501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG TO1 TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATTA CGCAATGGCC T51 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA B01 AAAACAGCTG GCGGAGGTG TCGCGAATAC GATTACCCCG CTGATGAAAG B51 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG GCCACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG TTTTTAGGTGG GGATGCCATT GCTCGGGTG AAATTTCGCT GGACGATGCG GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGCC AGGGTATTCG 101 TATGCTGGAT ACTGGCCACA GCTGACGGC CGGCCTGCCG CTACAGGTAC CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTAT TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTG CACAACGCGT CTTTACGCCA ACGCCAGCAT CGGTCTTTTT GGTGCGCGTG CACAACGCGT CTTTACGCCA ACGCCAGCAT CGGTCTTTTT GGTGCGCGTG CACAACGCGT CTTTACGCCA ACGCCAGCAT CGGTCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGG CCCTATGAGC CGGAAACCGG GTGCCATT CGCCGGTAT CCCCTAGGGACACC CCTATGAGC CGAAAGCGG GTGCCGTTT CGCCGGTAT GCTGGATGCA CCATACCTGG CGGTAAACC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG CGGTAAAACC CAACGTCGA GATATGGCA ACTGGGTCAT GCCTATGAGC CGGTAAAACC CAACGTCGA GATATGGCA ACTGGGTCAT GCCTAACCTGG CGCCGGAGA ACGTTGCTGA GATATGGCA ACTGGGTCAT GCGCATAGC CGCAGGCGC TACTGGCGTA TCGCCTCACTT AAGCAGGGCA TCGCGCTGGC CGCAAACCATG CGCCGGAGA ACGTTGCTGA TCGCCTCACTT AAGCAGGGCA TCGCGCTGGG CGCAAACCATG CGCGCGGAGA CCATGGCGTA TCGCCTCACTT AAGCAGGGCA TCGCGCTGGG CGCAAACCATG CGCGCGGAGA CCATGGCGTA TCGCCTCACTT AAGCAGGGCA TCGCGCTGGG CGCAAACCATG CGCGCGAGA CCATGGCGTA TCGCCCACAC CGGTGGTCAT CTGGCCTGGG CGCAAACCATG CGCCGGAGA CCATGGCGTA TCGCCCACAC CGGTGGTCACAC CGGCAAACCATG CGCGCGGGGT TACTGGCGTA TCGCCCACAC CGGTGGTCACAC CGGCAAACCATG CGGCAAACCATG GAGGCCAACA CGGTGGTCACAC CGGCAAACCAC CGGCCTGGGC CTGGCCTGGG GAGGCCAACA CGGTGGTCACAC CGGCCTGGC CTGGCCGGGT TACTGGCGTA AACCGGCC TTGCCCCGTG GAGGCCAACA CGGGGCTCT ACTGGCGGGT CTGGCCTGGAAACAC CGGGCCC TACTGAAACAC CGGCGCTCT ACTGGCGGGT CTGGCCGGGT AACGGGCCACAC CGGTGGTCACAC CGGCGCGCTTACCACGGC CTGGCGGGT AACGGGCCACAC CGGGGGCCACAC CGGGGGTCT ACTGGCGGGT CTGGCCGGGC AAACCGGCC GTTGCCCGGG CGCGTTGACCACCGGC CTGGCGGAAACAC CGGGCCACAC CG	551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATTA CGCAATGGCC TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG GCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG CTGATGAAAG CCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG CTGATGAGAC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG CTGATGAGAC CTGTCGAGC CTGTCGAGC AAACTTCGCT GGACGATGCG CTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGC AGGGTATCG CTGGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGC CTACAGGTAC CTGGATGAGGT CACCGACACACCGCT CTGCCCTGC CTACAGGTAC CTGGACGAGT CACCGACACACCGCT CTTCACGCCA ACGCCAGCAT CTGGCCGAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT CAGCCGCAGT GGACGCGGGTC CTTAAGCCGC TCAAGCTGG CCCTATGAGC CTTAACCTGG GACGCGGGTC CTTAAGCCGC TCAAGCTGG CCTATCGGC CTTAAGCCGC CTAACCTGG CTTAACCTGG CACAACCGCT TACGCCTGG GCTATCCTGG CTTAAGCCGC CTAACCTGG CTTAAGCCGC TCAAGCTTGG CTGGATAAACC GGTGCGCGTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG CGGTAAAGC GACGCGGGTC CTTAAGCCGC TCAAGCCTGG GCTATCGTGA CGGTAAAGCC GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG CGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGG CTATCGTGG CGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGG CTGGCCTGGG CTGGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGG CTGGCCTGGG CACACCGGCC TACTGGCCGC GAGAGCCAACA CGGTGGTCA CTGGGCTGGG	601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
751TACTGGGGTCAGGGCACCTCTGTTACCGTTTCTAGCACACCGGTGTCAGA801AAAACAGCTGGCGGAGGTGGTCGCGAATACGATTACCCCGCTGATGAAAG851CCCAGTCTGTTCCAGGCATGGCGGTGGCCGTTATTTATCAGGGAAAACCG901CACTATTACACATTTGGCAAGGCCGATATCGCGGCGAATAAACCCGTTAC951GCCTCAGACCCTGTTCGAGCTGGGTTCTATAAGTAAAACCTTCACCGGCG1001TTTTAGGTGGGGATGCCATTGCTCGCGGTGAAATTTCGCTGGACGATGCG1051GTGACCAGATACTGGCCACAGCTGACGGGCAAGCAGTGCAGGGTATTCG1101TATGCTGGATCTCGCCACCTACACCGCTGGCGGCCTGCCGCTACAGGTAC1151CGGATGAGGTCACGGATAACGCCTCCCTGCTGCGCTTTTATCAAAACTGG1201CAGCCGAGTGGAAGCCTGGCACAACGCGTCTTTACGCCAACGCCAGCAT1301AGGCCATGACGACGCGGGTCCTTAAGCCGCTCAAGCTGGACCATACCTGG1351ATTAACGTGCCGAAAGCGGAAGAGGCGCATTACGCCTGGGGCTATCGTGA1451GCGTGAAAACCAACGTGCAGGATATGGCGAACTGGGTCATGCTGGCTATG1451GCGCCGGAGAACGTTGCTGATGCCTCACTTAAGCAGGCATCGGGTCAT1551GCAGTCGCGTACTGGCGTATCGGGTCAATGTATCAGGGTCTGGGCTGGG1561GGTAATGTAGCACTGGCCCGTTGCCCGTGGCAGAAGTGAATCCACCGGC1701TCCCCCGGTCAAAGCGTCTAGGGCCAAACACGGTGGTCTAACTGGCGGT1751TTGGCAGATACACTGGCCTTTA	651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG 851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG 901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATGCG 1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG 1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC 1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAACC GACGCGGTT CGCCGGGTAT GCCTGGG GCTATCGTGA 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGC TCGCGCTTGCG 1551 GCAGTCGCC TACTGGCGTA TCGGGTCAAT GCCGGGTCAT 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGG 1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTCAA GCCGAGTTTT 1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC 1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACCGGCTCT ACTGGCGGTTTT 1651 TTGGCAGCTA CGTGGCCCTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1751 TTGGCAGCTA CAGGCTCTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1801 CTCGCGAATA CAAGCTTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA	701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG 901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATGCG 1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG 1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC 1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCG TACTGGCGTA TCGGGTCAAT GTATCAGGGT 1561 GGAATGTAG CACTGGCGC GTTGCCCGTG GCAGAAGTGA ACCAGGGTTTT 1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC 1701 TCCCCCGGTC AAAGCGTCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT 1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1801 CTCGCGAATA CAAGCTTATC GAACCCGGCA CGCGTTGAGG CGGCATACCA	751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC 951 GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATGCG 1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGCC AGGGTATTCG 1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC 1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCCTATGAGC 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGC GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCA GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGAAAG
951 GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG 1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATGCG 1051 GTGACCAGAT ACTGGCCACA GCTGACGGC AAGCAGTGGC AGGGTATTCG 1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC 1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAACC GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG	TTATTTATCA	GGGAAAACCG
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATGCG 1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG 1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC 1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGC 1601 AGATGCTCAA CTGGCCCTG GAGGCCAACA CGGTGGTCGA GACGAGTTTT 1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC 1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGT 1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1801 CTCGCGGAATA CAAGCTTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA	901	CACTATTACA	CATTTGGCAA	GGCCGATATC	GCGGCGAATA	AACCCGTTAC
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG 1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC 1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCCGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCG TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC 1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG 1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT 1251 CGGTCTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCCGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG	CTACAGGTAC
1251 CGGTCTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC 1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	TCAAAACTGG
AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG 1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	ACGCCAGCAT
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA 1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG		CGGTCTTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG	CCCTATGAGC
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG 1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	CCATACCTGG
1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG 1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG	GCTATCGTGA
1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC 1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	CAAGCCTATG
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG	1451	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT	GGCAAACATG
AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTCGA GACGAGTTTT 1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC 1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT 1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA	1501	GCGCCGGAGA	ACGTTGCTGA	TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC 1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT 1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA	1551	GCAGTCGCGC	TACTGGCGTA	TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT 1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA	1601	AGATGCTCAA	CTGGCCCGTG	GAGGCCAACA	CGGTGGTCGA	GACGAGTTTT
1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG 1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA	1651	GGTAATGTAG	CACTGGCGCC	GTTGCCCGTG		ATCCACCGGC
1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA		TCCCCCGGTC	AAAGCGTCCT		•	ACTGGCGGGT
		TTGGCAGCTA				TATTGTGATG
1851 TATCCTCGAG GCGCTACAG (SEQ ID NO:9)		CTCGCGAATA			CGCGTTGAGG	CGGCATACCA
	1851	TATCCTCGAG	GCGCTACAG	(SEQ ID NO:9)		

FIG._4B

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1_	DIVLTOSPAS	L S VSLGQRAT	MSCRAGESVD	IFGVGFLHWY	OOKPGOPPKL
51	LIYRASNLES	GIPVRFSGTG	SGTDFTLIID	PVEADDVATY	YCQQTNEDPY
101	TFGGGTKLEI	K <i>GGGGSGGG</i>	SGGGGSGGG	SGGGGSGGG	
<u>151</u>	ELVEPGASVK	LSCTASGFNI			RIDPANGNSK
201	YVPKFQGKAT	ITADTSSNTA	YLOLTSLTSE	DTAVYYCAPF	
251	YWGQGTSVTV			LM A AQSVPGM	
301				FTGVLGGDAI	
351				LQVPDEVTDN	
401			GALAVKPSGM		
451			VRVSPGMLDA		DMANWVMANM
501	APENVADASL				EANTVVETSF
551	GNVALAPLPV		KASWVHKTGS		IPEKQIGIVM
601	LANTSYPNPA		ALQ (SEQ ID !		

FIG._4C

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1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGCG
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACÄA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGGCGG
851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG	TTATTTATCA	GGGAAAACCG
901	CACTATTACA	CATTTGGCAA	GGCCGATATC	GCGGCGAATA	AACCCGTTAC
951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG	CTACAGGTAC
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	TCAAAACTGG
1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	ACGCCAGCAT
1251	CGGTCTTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG	CCCTATGAGC
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	CCATACCTGG
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG	GCTATCGTGA
1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	CAAGCCTATG
1451	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT	GGCAAACATG
1501	GCGCCGGAGA	ACGTTGCTGA	TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1551	GCAGTCGCGC	TACTGGCGTA	TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1601	AGATGCTCAA	CTGGCCCGTG	GAGGCCAACA	CGGTGGTCGA	GACGAGTTTT
1651	GGTAATGTAG	CACTGGCGCC	GTTGCCCGTG	GCAGAAGTGA	ATCCACCGGC
1701	TCCCCCGGTC	AAAGCGTCCT	GGGTCCATAA	AACGGGCTCT	ACTGGCGGGT
1751	TTGGCGCGTA	CGTGGCCTTT	ATTCCTGAAA	AGCAGATCGG	TATTGTGATG
1801	CTCGCGAATA	CAAGCTATCC		CGCGTTGAGG	CGGCATACCA
1851	TATCCTCGAG	GCGCTACAG (SEQ ID NO:10)	

FIG._4D

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					•
1	AGGAATTATC	ATATGAAATA	CCTGCTGCCG	ACCGCTGCTG	CTGGTCTGCT
51	GCTCCTCGCT	GCCCAGCCGG	CCATGGCCGA	CATCGTCCTG	ACCCAGAGCC
101	CGGCAAGCCT	GTCTGTTTCC	CTGGGCCAGC	GTGCCACTAT	GTCCTGCAGA
151	GCGGGTGAGT	CTGTTGACAT	TTTCGGTGTC	GGTTTTCTGC	ACTGGTACCA
201	ACAGAAACCG	GGTCAGCCGC	CAAAACTGCT	GATCTATCGT	GCTTCTAACC
251	TGGAGTCCGG	CATCCCGGTA	CGTTTCTCCG	GTACTGGCTC	TGGTACTGAT
301	TTTACCCTGA	TTATCGACCC	GGTGGAAGCA	GACGATGTTG	CCACCTACTA
351	TTGCCAGCAG	ACCAACGAGG	ATCCGTACAC	CTTCGGTGGC	GGTACTAAAC
401	TGGAGATCAA	AGGCGGTGGT	GGTTCTGGTG	GTGGTGGTAG	CGGTGGCGGT
451	GGTAGCGGTG	GCGGTGGCAG	CGGTGGTGGT	GGCTCTGGTG	GCGGTGGCTC
501	TGAAGTGCAG	CTGCAGCAGT	CCGGTGCGGA	GCTCGTTGAA	CCGGGCGCTT
551	CTGTGAAACT	GTCTTGCACT	GCATCTGGTT	TCAACATTAA	GGACACCTAC
601	ATGCACTGGG	TGAAACAACG	-	GGTCTGGAGT	
651	CATCGATCCG	GCTAACGGTA	- -	CGTGCCAAAA	TTCCAGGGTA
701	AAGCAACCAT	CACTGCTGAT			
751	ACTTCCCTGA	CTAGCGAAGA			CTCCGTTCGG
801	CTACTATGTC	AGCGATTACG		CTGGGGTCAG	
851	TTACCGTTTC	TAGCACACCG	GTGTCAGAAA	AACAGCTGGC	GGAGGTGGTC
901	GCGAATACGA	TTACCCCGCT	GATGGCGGCC	CAGTCTGTTC	CAGGCATGGC
951	GGTGGCCGTT	ATTTATCAGG	GAAAACCGCA	CTATTACACA	0-1-0-1-1-0-0-0
1001	CCGATATCGC	GGCGAATAAA			GTTCGAGCTG
1051	GGTTCTATAA	GTAAAACCTT	CACCGGCGTT	TTAGGTGGGG	ATGCCATTGC
1101	TCGCGGTGAA		ACGATGCGGT	GACCAGATAC	TGGCCACAGC
1151	TGACGGGCAA	GCAGTGGCAG	GGTATTCGTA		CGCCACCTAC
1201	ACCGCTGGCG	GCAGIGGCAG	ACAGGTACCG		CGCACCTAC
	CTCCCTGCTG	CGCTTTTATC	AAAACTGGCA	GCCGCAGTGG	AAGCCTGGCA
1251					
1301	CAACGCGTCT	TTACGCCAAC	GCCAGCATCG	GTCTTTTTGG	TGCGCTGGCG
1351	GTCAAACCTT	CTGGCATGCC	CTATGAGCAG	_	CGCGGGTCCT
1401	TAAGCCGCTC	AAGCTGGACC	ATACCTGGAT		AAAGCGGAAG
1451	AGGCGCATTA	CGCCTGGGGC	TATCGTGACG	GTAAAGCGGT	GCGCGTTTCG
1501	CCGGGTATGC		AGCCTATGGC		ACGTGCAGGA
1551	TATGGCGAAC		CAAACATGGC		GTTGCTGATG
1601	CCTCACTTAA		GCGCTGGCGC		
1651		ATCAGGGTCT			
1701		GTGGTCGAGA			
1751		AGAAGTGAAT			
1801		CGGGCTCTAC			
1851	TCCTGAAAAG	CAGATCGGTA	TTGTGATGCT	CGCGAATACA	AGCTATCCGA
1901	ACCCGGCACG	CGTTGAGGCG	GCATACCATA	TCCTCGAGGC	GCTACAGTAG
1951	GAATTCGAGC	TCCGTCGACA	AGCTTGCGGC	CGCACTCGAG	ATCAAACGGG
2001	CTAGCCAGCC	AGAACTCGCC	CCGGAAGACC	CCGAGGATGT	CGAGCACCAC
2051	CACCACCACC	ACTGAGATCC	GGCTGCTAAC	AAAGCCCGAA	AGGAAGCTGA
2101	GTTGGCTGCT	GCCACCGCTG	AGCAATAACT	AGCATAACCC	CTTGGGGCCT
2151	CTAAACGGG'T	CTTGAGGGGT	TTTTTGCTGA	AAGGAGGAAC	TATATCCGGA
2201	TTGGCGAATG	GGACGCGCCC	TGTAGCGGCG	CATTAAGCGC	GGCGGGTGTG
2251	GTGGTTACGC	GCAGCGTGAC	CGCTACACTT	GCCAGCGCCC	TAGCGCCCGC
2301	TCCTTTCGCT	TTCTTCCCTT	CCTTTCTCGC	CACGTTCGCC	GGCTTTCCCC

FIG._4E-1

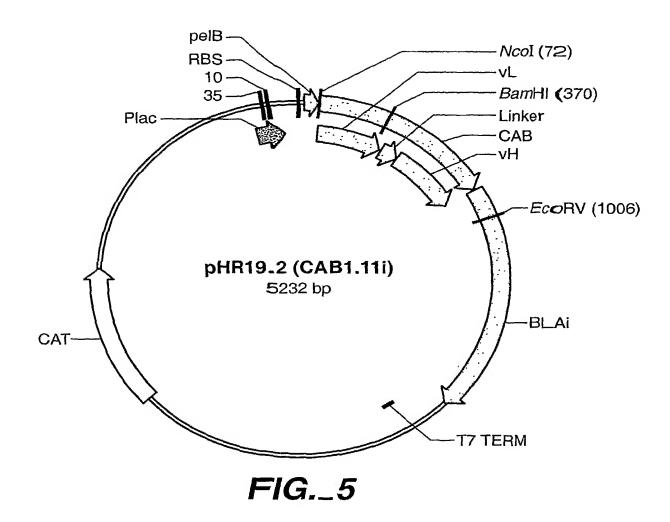
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2351		AAATCGGGGG			TAGTGCTTTA
2401			ACTTGATTAG	GGTGATGGTT	CACGT.AGTGG
2451	GCCATCGCCC		TTTTTCGCCC	TTTGACGTTG	GAGTC CACGT
2501	TCTTTAATAG		TTCCAAACTG	GAACAACACT	CAACC CTATC
2551	TCGGTCTATT		ATAAGGGATT	TTGCCGATTT	CGGCC TATTG
2601	GTTAAAAAAT	GAGCTGATTT	AACAAAAATT	TAACGCGAAT	TTTAACAAAA
2651	TATTAACGCT		TGATGCGGTA	TTTTCTCCTT	ACGCATCTGT
2701		ACACCGCATA	TGGTGCACTC	TCAGTACAAT	CTGCTCTGAT
2751	GCCGCATAGT	TAAGCCAGCC	CCGACACCCG	CCAACACCCG	CTGACGCGCC
2801	CTGACGGGCT	TGTCTGCTCC	CGGCATCCGC	TTACAGACAA	GCTGTGACCG
2851	TCTCCGGGAG	CTGCATGTGT	CAGAGGTTTT	CACCGTCATC	ACCGA_AACGC
2901	GCGAGACGAA	AGGGCCTCGT	GATACGCCTA	TTTTTATAGG	TTAATGTCAT
2951	GATAATAATG	GTTTCTTAGA	CGTCAGGTGG	CACTTTTCGG	GGAAATGTGC
3001	GCGGAACCCC	TATTTGTTTA	TTTTTCTAAA	TACATTCAAA	TATGTATCCG
3051	CTCATGAGAC	AATAACCCTG	TGGCAGCATC	ACCCGACGCA	CTTTGCGCCG
3101	AATAAATACC	TGTGACGGAA	GATCACTTCG	CAGAATAAAT	AAATCCTGGT
3151	GTCCCTGTTG	ATACCGGGAA	GCCCTGGGCC	AACTTTTGGC	GAAAATGAGA
3201	CGTTGATCGG	CACGTAAGAG	GTTCCAACTT	TCACCATAAT	GAAATAAGAT
3251	CACTACCGGG	CGTATTTTTT	GAGTTATCGA	GATTTTCAGG	AGCTAAGGAA
3301	GCTAAAATGG	AGAAAA AAT	CACTGGATAT	ACCACCGTTG	ATATATCCCA
3351	ATGGCATCGT	AAAGAACATT	TTGAGGCATT	TCAGTCAGTT	GCTCAATGTA
3401	CCTATAACCA	GACCGTTCAG	CTGGATATTA	CGGCCTTTTT	AAAGACCGTA
3451	AAGAAAAATA	AGCACAAGTT	TTATCCGGCC	TTTATTCACA	TTCTTGCCCG
3501	CCTGATGAAT	GCTCATCCGG	AATTCCGTAT	GGCAATGAAA	GACGGTGAGC
3551	TGGTGATATG	GGATAGTGTT	CACCCTTGTT	ACACCGTTTT	CCAT GAGCAA
3601	ACTGAAACGT	TTTCATCGCT	CTGGAGTGAA	TACCACGACG	ATTT CCGGCA
3651	GTTTCTACAC	ATATATTCGC	AAGATGTGGC	GTGTTACGGT	GAAA ACCTGG
3701	CCTATTTCCC	TAAAGGGTTT	ATTGAGAATA		CTCAGCCAAT
3751	CCCTGGGTGA	GTTTCACCAG	TTTTGATTTA		ATATGGACAA
3801	CTTCTTCGCC	CCCGTTTTCA	CGATGGGCAA		CAAG-GCGACA
3851	AGGTGCTGAT	GCCGCTGGCG	ATTCAGGTTC		CTGTGATGGC
3901	TTCCATGTCG	GCAGAATGCT	TAATGAATTA		GCGATGAGTG
3951	GCAGGGCGGG	GCGTAAAGAC	AGATCGCTGA		
4001	AGCATTGGTA	ACTGTCAGAC			
4051		ATTTTTAATT			
4101		ACCAAAATCC			
4151		AGAAAAGATC			
4201		GCTGCTTGCA			
4251		GATCAAGAGC	TACCAACTCT		
4301		GCAGATACCA			
4351		TCAAGAACTC			
4401					
4451		CCAGTGGCTG			
4501		AAGACGATAG			
4551		CGTGCACACA			
4601		CTACAGCGTG			
4651		GGACAGGTAT			
#00T	UUUAUUAJUU	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT	ATAGTCCTGT

FIG._4E-2

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4701	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA	TGCTCGTCAG
4751	GGGGGCGGAG	CCTATGGAAA	AACGCCAGCA	ACGCGGCCTT	TTTACGGTTC
4801	CTGGCCTTTT	GCTGGCCTTT	TGCTCACATG	TTCTTTCCTG	CGTTATCCCC
4851	TGATTCTGTG	${\tt GATAACCGTA}$	TTACCGCCTT	TGAGTGAGCT	GATACCGCTC
4901	GCCGCAGCCG	AACGACCGAG	CGCAGCGAGT	CAGTGAGCGA	GGAAGCGGAA
4951	GAGCGCCCAA	TACGCAAACC	GCCTCTCCCC	GCGCGTTGGC	${\tt CGATTCATTA}$
5001	ATGCAGCTGG	CACGACAGGT	TTCCCGACTG	GAAAGCGGGC	${\tt AGTGAGCGCA}$
5051	ACGCAATTAA	TGTGAGTTAG	CTCACTCATT	AGGCACCCCA	${\tt GGCTTTACAC}$
5101	TTTATGCTTC	CGGCTCGTAT	${\tt GTTGTGTGGA}$	ATTGTGAGCG	${\tt GATAACAATT}$
5151	TCACACAGGA	AACAGCTATG	ACCATGATTA	CGCCAAGCTA	TTTAGGTGAC
5201	ACTATAGAAT	ACTCAAGCTT	TCTAGATTAA	GG	

FIG._4E-3



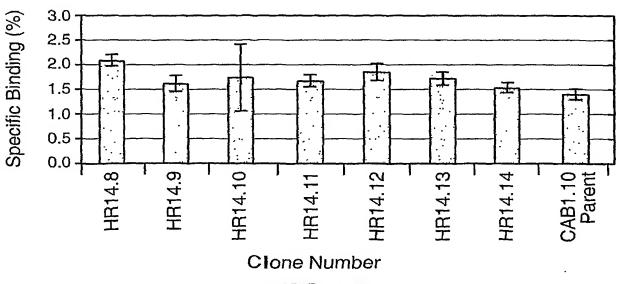


FIG._6

ADEPT 14L; EB101.1/pHR19.2, CAB1.11i

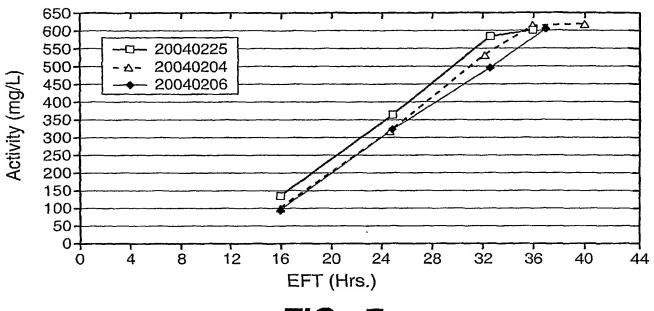


FIG._7

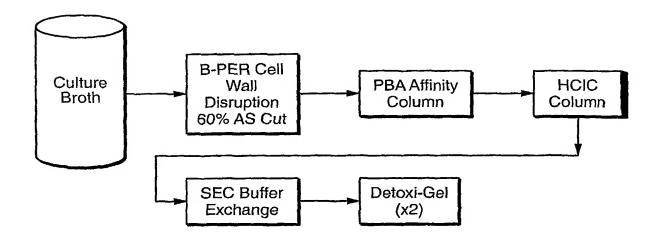


FIG._8

Lane 1: Molecular Weight Standard; Lanes 3-5: Unrelated Proteins; Lane 6: CAB1.11i.

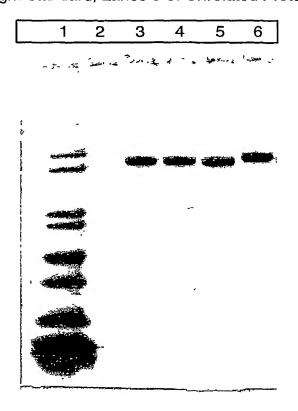
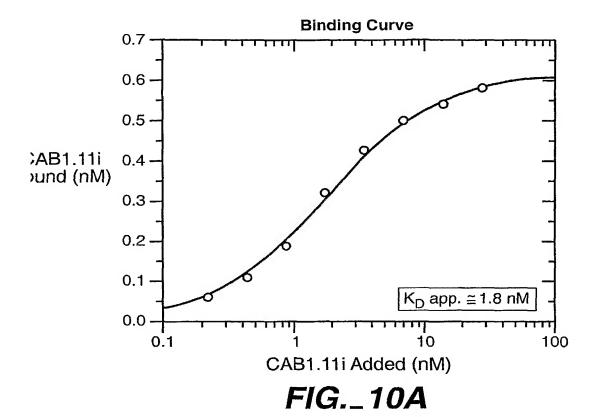
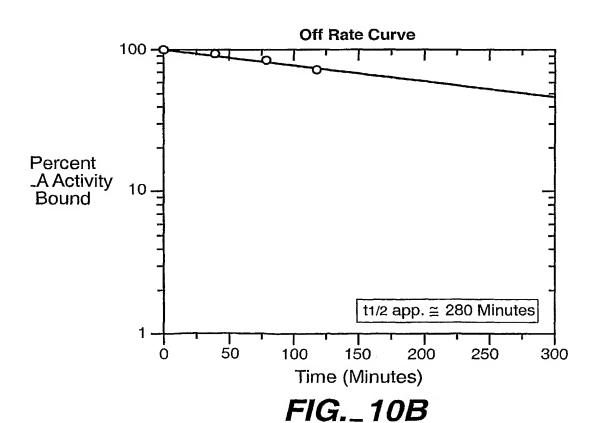
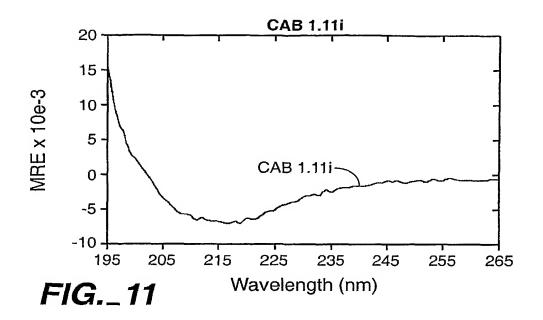


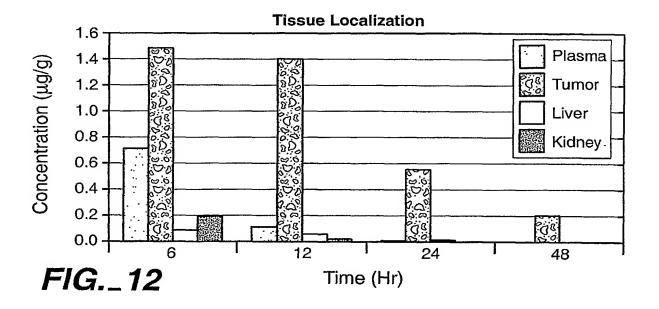
FIG._9

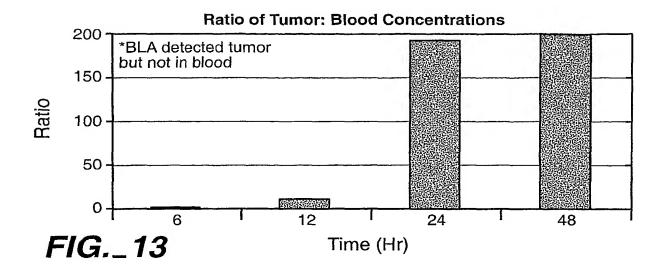




SUBSTITUTE SHEET (RULE 26)







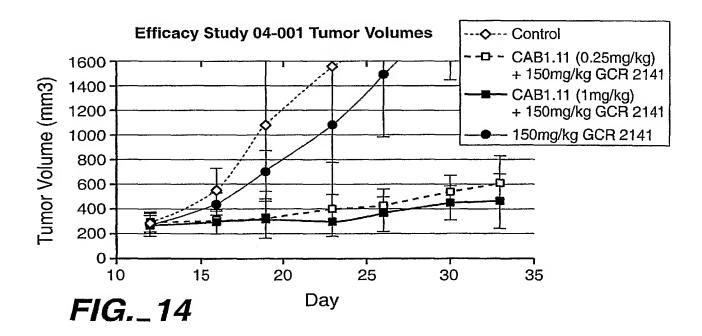


FIG._15A

Case ID	ASM	Sample ID	Sample Pathology
<u>Cl0000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
<u>Cl0000005496</u>	FF5	FR5B337147	Adenocarcinoma of lung
CI0000011577	FF1	FR5B34059F	Adenocarcinoma of lung
<u>CI7000000241</u>	ÅF4	FR00033A78	Adenocarcinoma of lung
<u>Cl0000007518</u>	AF5	FR0001FD15	Carcinoma of lung, squa mous cell
<u>Cl000008475</u>	HF4	FR65EE0784	Adenocarcinoma of colon, metastatic
<u>Cl0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

FIG._15B

Case Diagnosis	Tissue of Origin/Site of Finding	H/E
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIB	Lung/Lung	<u>4X 20X</u>
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X 20X</u>
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung '	<u>4X 20X</u>
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of colon, metastatic Grade: Not Reported Stage: IV	Colon/Liver	<u>4X 20X</u>
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	<u>4X</u> <u>20X</u>
OUDOTITUTE	I CUEET (DIII E 26)	, J

FIG._15C

Anti-Human Cytokeratin AE1/AE3	CAB/GCR3708 (0.2ug/ml)
Immunogencity: Tumor (100%, Variable to 3+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029758	Immunogencity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High 4x 20x SF00029756
	Immunogencity: Tumor (15%, Variable to 3+ Cyto) Intra-alveolar macro phages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High 4x SF0002975B
	Immunogencity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High 4x 20x SF0002977F
	Immunogencity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High 4x 20x SF0002978B
	Immunogencity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF0002975F
Immunogencity: Tumor (98%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (2+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF0002976A	Immunogencity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029768 Normal liver parenchyma shows positive staining (1+)
	Immunogencity: Tumor (85%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High 4x SF00029783

FIG._15D

CAR/COREETZ /O Over/coll	CAR/COROTOR (O.S. 1. 1)
CAB/GCR5517 (0.2ug/ml)	CAB/GCR6798 (0.2ug/ml)
Immunogencity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 3+ Cyto) Necrosis (Variable to 2+ EC) Specificity: High 4x 20x	Immunogencity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High 4x 20x SF00029753
<u>SF00029757</u>	
Immunogencity: Tumor (40%, Variable to 3+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High 4x 20x SF0002975C	Immunogencity: Tumor (10%, Variable to 2+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029759
Immunogencity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High 4x 20x SF00029780	Immunogencity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High . 4x SF0002977D
Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC)	Immunogencity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029789
Immunogencity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x SF00029760	Immunogencity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975D</u>
	Immunogencity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029765 Normal liver parenchyma shows positive staining (1+)
Immunogencity: Tumor (85%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High 4x SF00029784	Immunogencity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High 4x SF00029781

FIG._15E

CAB/GCR8886 (0.196ug/ml)	No Antibody Control (Prediluted)
Immunogencity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High 4x 20x SF00029754	Immunogencity: N/A Specificity: Unknown <u>SF00029755</u>
Immunogencity: Tumor (10%, Variable to 2+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High 4x 20x SF0002975A Immunogencity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory:cells (Variable to 1+ Cyto)	
Specificity: High 4x 20x SF0002977E Immunogencity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High	
Immunogencity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x	
Immunogencity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029766 Normal liver parenchyma shows positive staining (1+) Immunogencity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto)	Immunogencity: N/A Specificity: Unknown SF00029767
Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029782	

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<u>Cl0000017970</u>	HF1	FR65EE7B3D	Adenocarcinoma of colon
<u>Cl0000010013</u>	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
<u>Cl000009651</u>	AF1	FR0002B111	Adenocarcinoma of pancreas, ductal
<u>C10000008690</u>	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u>Cl000007678</u>	AF3	FR0002575B	Adenocarcinoma of pancreas, ductal
<u>Cl0000009736</u>	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

FIG._15F

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Adenocarcinoma of colon Grade: AJCC G3: Moderately differentiated Stage: IIIC	Colon/Colon	4X 2OX
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X 2OX</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>AX 20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	<u>4X</u> 2 • 0X
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: III	Pancreas/Pancreas	4X 20X
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>≥0X</u>

FIG._15G

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	Immunogencity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029787
Immunogencity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 1+ Cyto) Specificity: High 4x SF0002977C	Immunogencity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High 4x 20x SF0002977A
	Immunogencity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High 4x SF00029771
	Immunogencity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High <u>4x</u> 20x SF0002976D
	Immunogencity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High 4x SF00029763
	Immunogencity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029775

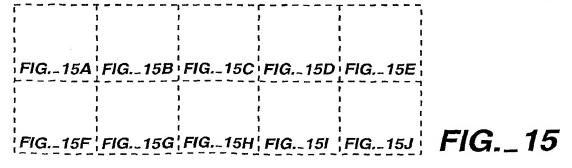
FIG._15H

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Immunogencity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x SF00029788	Immunogencity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029785
Immunogencity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High 4x 20x SF0002977B	Immunogencity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029777
Immunogencity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029772	Immunogencity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High 4x SF00029770
Immunogencity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High 4x SF0002976E	Immunogencity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002976B</u>
Immunogencity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High 4x SF00029764	Immunogencity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High 4x 20x SF00029761
Immunogencity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029776	Immunogencity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Specificity: High 4x 20x SF00029773

FIG._151

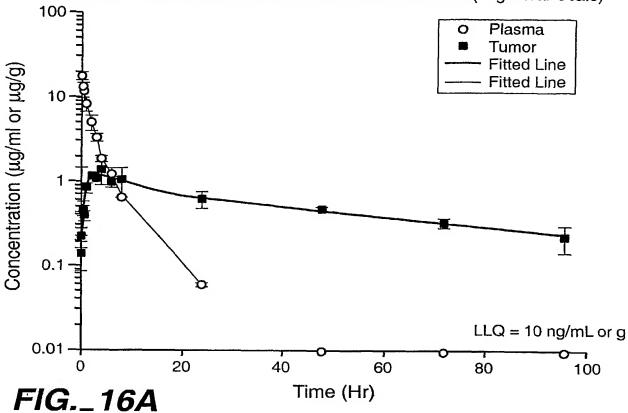
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Immunogencity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029786	
Immunogencity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029778	Immunogencity: N/A Specificity: N/A <u>SF00029779</u>
Immunogencity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High 4x SF0002976F	
Immunogencity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High 4x 20x SF0002976C	
Immunogencity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High 4x 20x SF00029762	
Immunogencity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High 4x 20x SF00029774	

FIG__15J

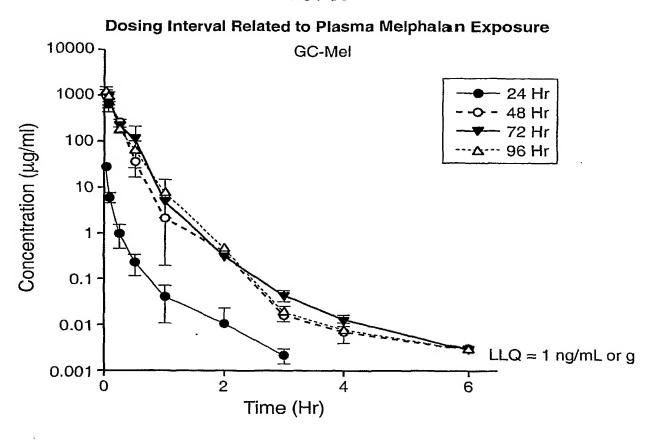


Eliminated from Plasma and Retained in Tumor to at Least 96 Hr

Plasma and Tumor GCR-8886 Concentration-time Profiles (Log-linear Scale)



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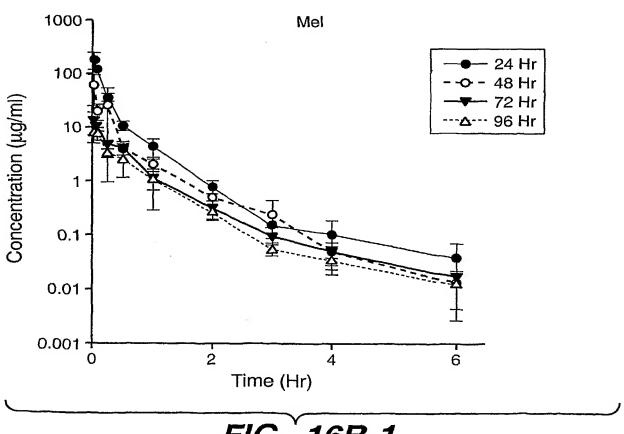
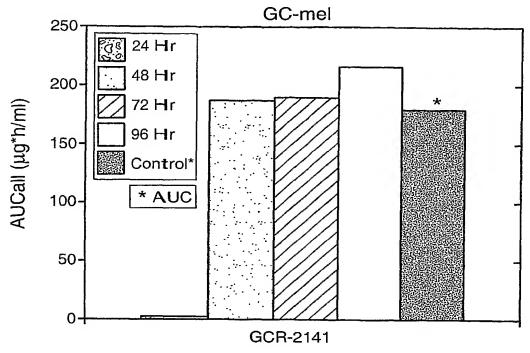
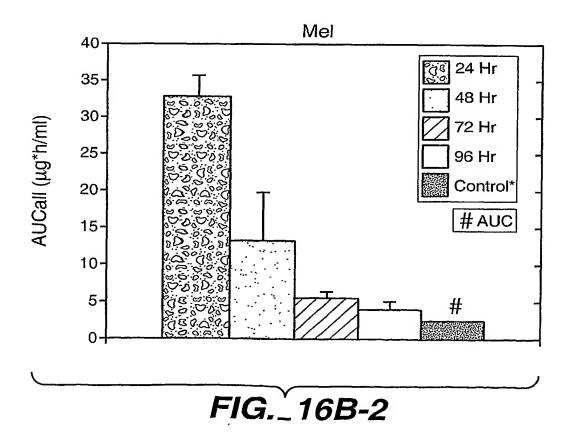


FIG._16B-1

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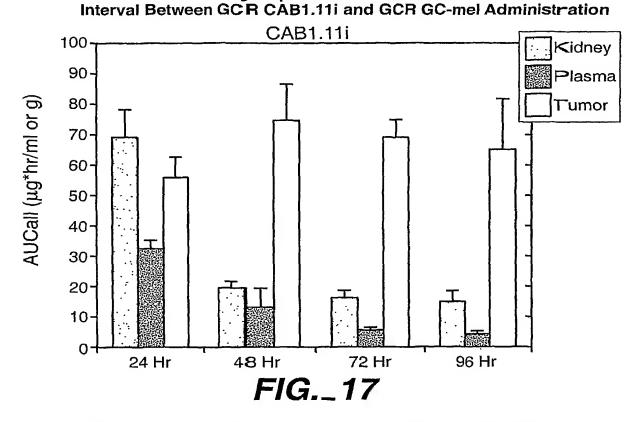
Dosing Interval Related to Plasma Melphalan Exposure



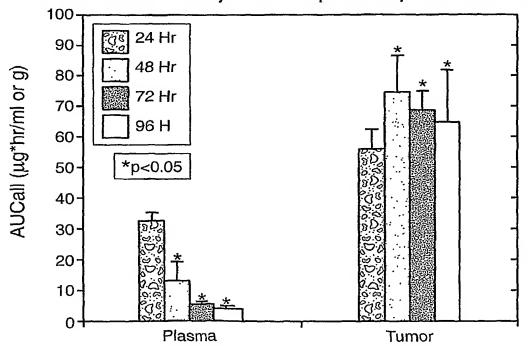


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Plasma and Kidney Exposure to is Decreased with Increased



Efficacious Tumor Melphalan Exposures Achieved at Each Time Interval While Systemic Melphalan Exposure Decreased



• Efficacy demonstrated at 24 hr interval in TLS174T xenograft mouse model

FIG._18

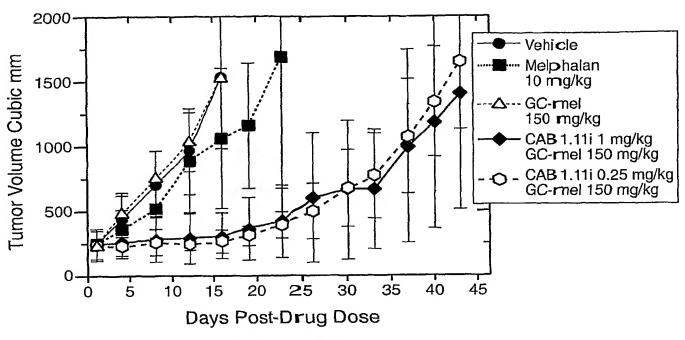
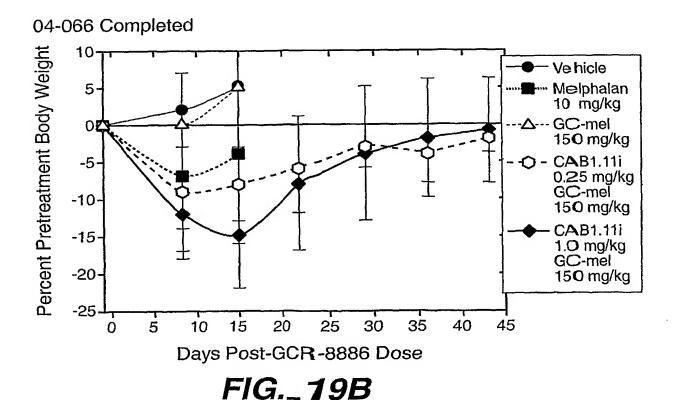


FIG._19A



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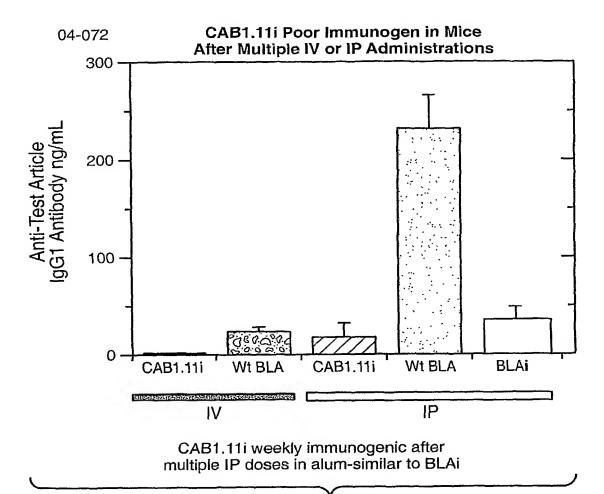


FIG._20

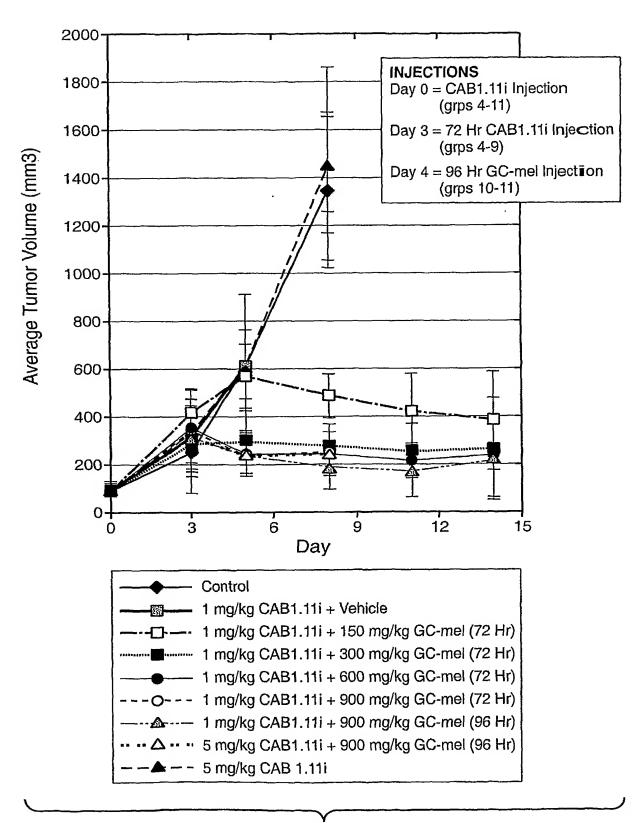


FIG._21

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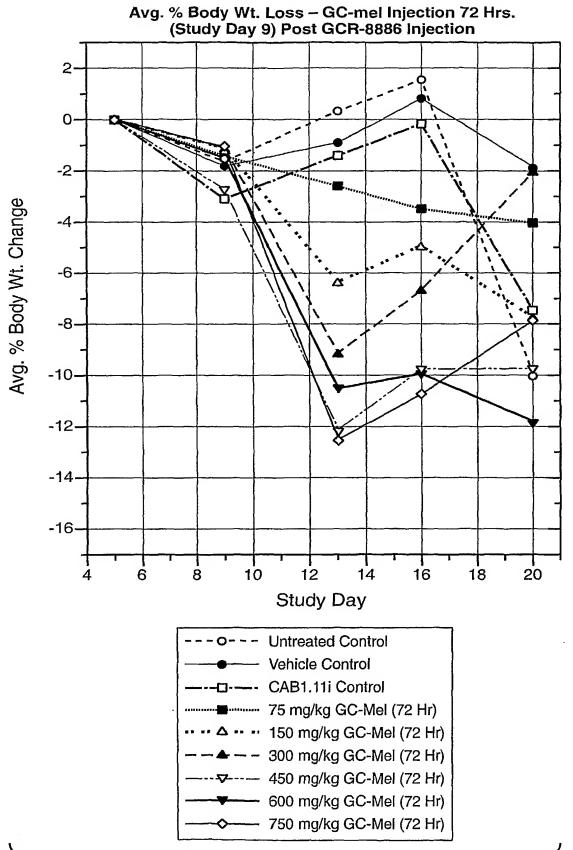


FIG._22A

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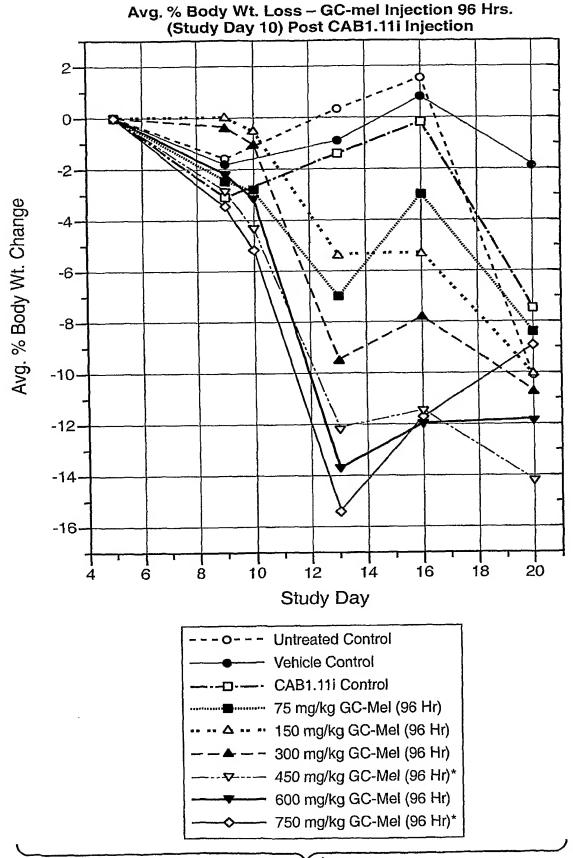


FIG. 22B

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Plasma CAB1.11i Concentration-time Profile in Rats
Results

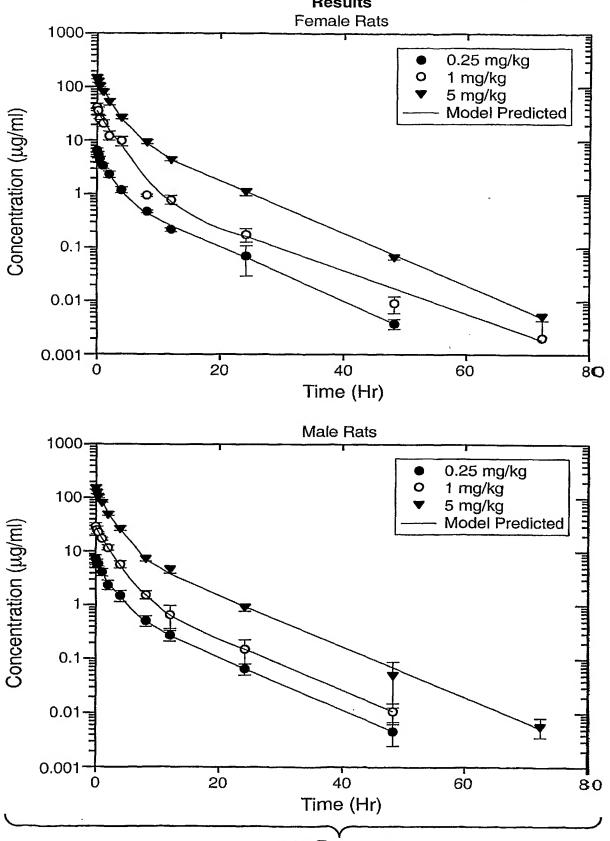
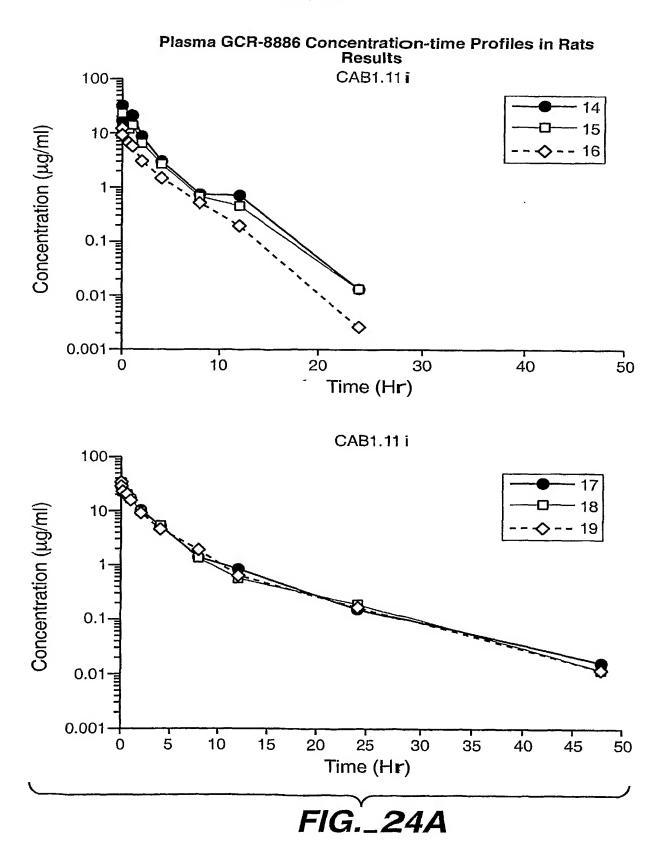


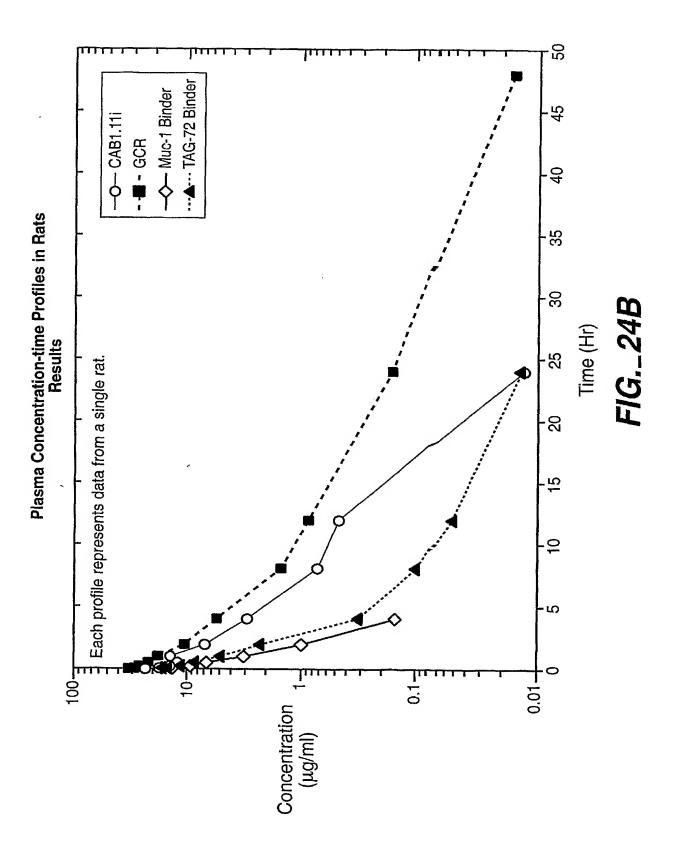
FIG._23

PCT/US2005/012270

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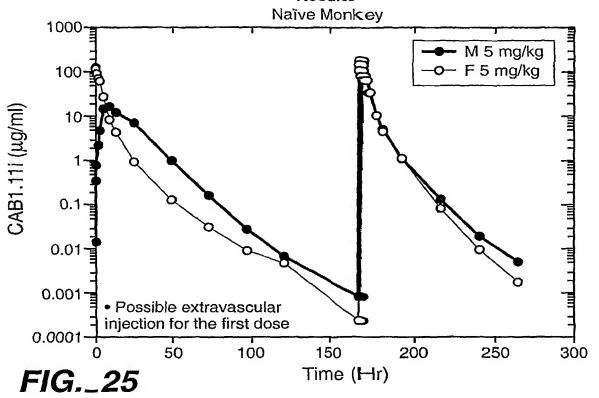


SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)

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GCR-8886 Concentration-time Profiles Following 2 Weekly Doses
Results



CAB1.11i PK Parameter Estimates with or without CEA Coadministration Results

